Full wwPDB X-ray Structure Validation Report (i)

Mar 7, 2022 – 04:44 PM EST

PDB ID	:	5SCC
Title	:	Structure of liver pyruvate kinase in complex with anthraquinone derivative 57
Authors	:	Lulla, A.; Foller, A.; Nain-Perez, A.; Grotli, M.; Brear, P.; Hyvonen, M.
Deposited on	:	2021-12-01
Resolution	:	1.89 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

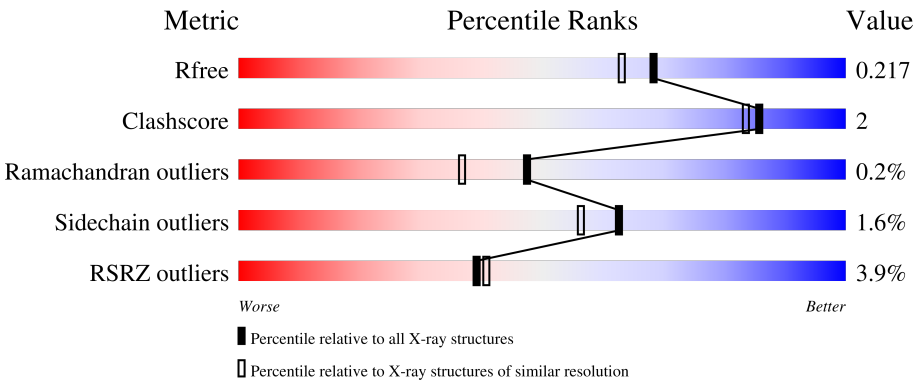
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.27
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	447	8% 87% 6% 6%
1	B	447	4% 91% 6% • •
1	C	447	2% 89% 6% 5%
1	D	447	2% 89% 5% • 5%
1	E	447	5% 89% 5% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	447	3% 89% 8%
1	G	447	4% 89% 5% 6%
1	H	447	2% 90% 5% 5%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 28866 atoms, of which 27 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Pyruvate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	419	3242	2035	582	605	20	0	13	0
1	B	436	3350	2104	604	622	20	3	8	0
1	C	424	3268	2058	584	607	19	0	9	0
1	D	424	3254	2043	589	603	19	0	8	0
1	E	419	3257	2049	584	604	20	0	13	0
1	F	432	3327	2094	597	616	20	0	8	0
1	G	422	3246	2042	582	603	19	0	8	0
1	H	424	3273	2055	596	603	19	0	9	0

There are 48 discrepancies between the modelled and reference sequences:

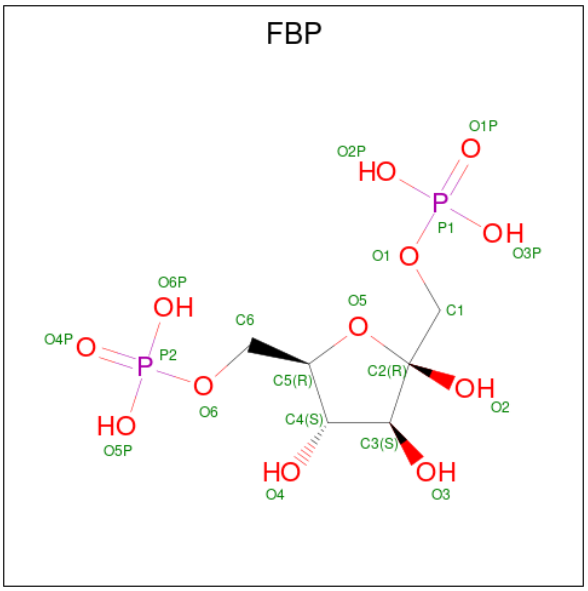
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q16716
A	0	SER	-	expression tag	UNP Q16716
A	12	ASP	SER	conflict	UNP Q16716
A	130	GLY	-	linker	UNP Q16716
A	131	SER	-	linker	UNP Q16716
A	132	GLY	-	linker	UNP Q16716
B	-1	GLY	-	expression tag	UNP Q16716
B	0	SER	-	expression tag	UNP Q16716
B	12	ASP	SER	conflict	UNP Q16716
B	130	GLY	-	linker	UNP Q16716
B	131	SER	-	linker	UNP Q16716
B	132	GLY	-	linker	UNP Q16716
C	-1	GLY	-	expression tag	UNP Q16716

Continued on next page...

Continued from previous page...

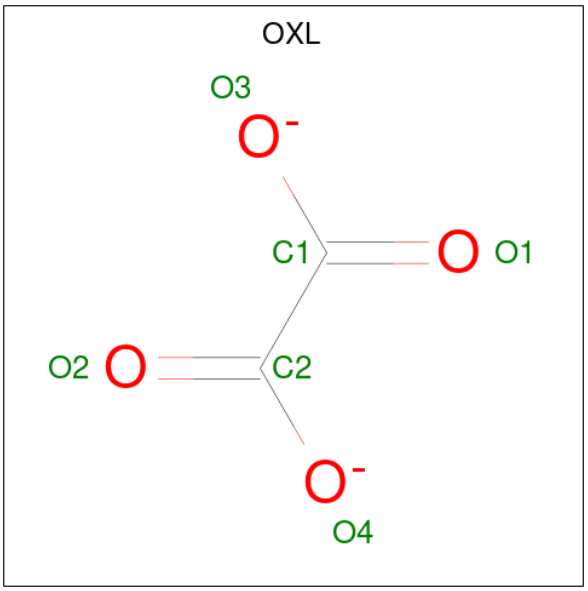
Chain	Residue	Modelled	Actual	Comment	Reference
C	0	SER	-	expression tag	UNP Q16716
C	12	ASP	SER	conflict	UNP Q16716
C	228	GLY	-	linker	UNP Q16716
C	229	SER	-	linker	UNP Q16716
C	230	GLY	-	linker	UNP Q16716
D	-1	GLY	-	expression tag	UNP Q16716
D	0	SER	-	expression tag	UNP Q16716
D	12	ASP	SER	conflict	UNP Q16716
D	130	GLY	-	linker	UNP Q16716
D	131	SER	-	linker	UNP Q16716
D	132	GLY	-	linker	UNP Q16716
E	-1	GLY	-	expression tag	UNP Q16716
E	0	SER	-	expression tag	UNP Q16716
E	12	ASP	SER	conflict	UNP Q16716
E	228	GLY	-	linker	UNP Q16716
E	229	SER	-	linker	UNP Q16716
E	230	GLY	-	linker	UNP Q16716
F	-1	GLY	-	expression tag	UNP Q16716
F	0	SER	-	expression tag	UNP Q16716
F	12	ASP	SER	conflict	UNP Q16716
F	228	GLY	-	linker	UNP Q16716
F	229	SER	-	linker	UNP Q16716
F	230	GLY	-	linker	UNP Q16716
G	-1	GLY	-	expression tag	UNP Q16716
G	0	SER	-	expression tag	UNP Q16716
G	12	ASP	SER	conflict	UNP Q16716
G	228	GLY	-	linker	UNP Q16716
G	229	SER	-	linker	UNP Q16716
G	230	GLY	-	linker	UNP Q16716
H	-1	GLY	-	expression tag	UNP Q16716
H	0	SER	-	expression tag	UNP Q16716
H	12	ASP	SER	conflict	UNP Q16716
H	130	GLY	-	linker	UNP Q16716
H	131	SER	-	linker	UNP Q16716
H	132	GLY	-	linker	UNP Q16716

- Molecule 2 is 1,6-di-O-phosphono-beta-D-fructofuranose (three-letter code: FBP) (formula: $C_6H_{14}O_{12}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
2	A	1	20	6	12	2	0	0
			Total	C	O	P		
2	B	1	20	6	12	2	0	0
			Total	C	O	P		
2	C	1	20	6	12	2	0	0
			Total	C	O	P		
2	D	1	20	6	12	2	0	0
			Total	C	O	P		
2	E	1	20	6	12	2	0	0
			Total	C	O	P		
2	F	1	20	6	12	2	0	0
			Total	C	O	P		
2	G	1	20	6	12	2	0	0
			Total	C	O	P		
2	H	1	20	6	12	2	0	0

- Molecule 3 is OXALATE ION (three-letter code: OXL) (formula: C_2O_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 2 4	0	0
3	B	1	Total C O 6 2 4	0	0
3	C	1	Total C O 6 2 4	0	0
3	D	1	Total C O 6 2 4	0	0
3	E	1	Total C O 6 2 4	0	0
3	F	1	Total C O 6 2 4	0	0
3	G	1	Total C O 6 2 4	0	0
3	H	1	Total C O 6 2 4	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mg 1 1	0	0
4	B	1	Total Mg 1 1	0	0
4	C	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0

Continued on next page...

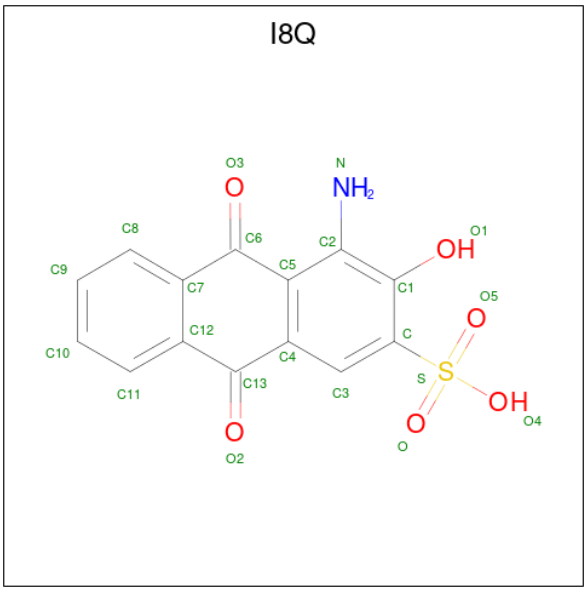
Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total Mg 1 1	0	0
4	F	1	Total Mg 1 1	0	0
4	G	1	Total Mg 1 1	0	0
4	H	1	Total Mg 1 1	0	0

- Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total K 1 1	0	0
5	B	1	Total K 1 1	0	0
5	C	1	Total K 1 1	0	0
5	D	1	Total K 1 1	0	0
5	E	1	Total K 1 1	0	0
5	F	1	Total K 1 1	0	0
5	G	1	Total K 1 1	0	0
5	H	1	Total K 1 1	0	0

- Molecule 6 is 4-amino-3-hydroxy-9,10-dioxo-9,10-dihydroanthracene-2-sulfonic acid (three-letter code: I8Q) (formula: $C_{14}H_9NO_6S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	S		
6	C	1	31	14	9	1	6	1	9	0
			Total	C	H	N	O	S		
6	F	1	31	14	9	1	6	1	9	0
			Total	C	H	N	O	S		
6	G	1	31	14	9	1	6	1	9	0

- Molecule 7 is water.

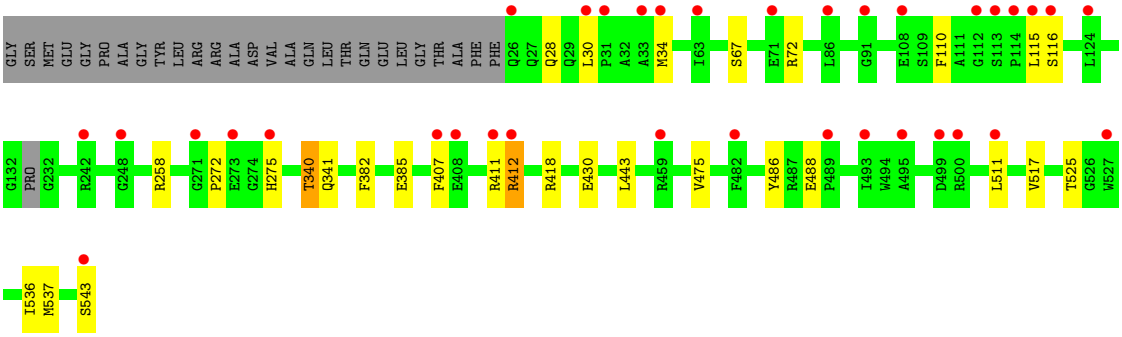
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	179	179	179	0	0
			Total	O		
7	B	209	209	209	0	0
			Total	O		
7	C	333	333	333	0	0
			Total	O		
7	D	368	368	368	0	0
			Total	O		
7	E	195	195	195	0	0
			Total	O		
7	F	286	286	286	0	0
			Total	O		
7	G	359	359	359	0	0
			Total	O		
7	H	403	403	403	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

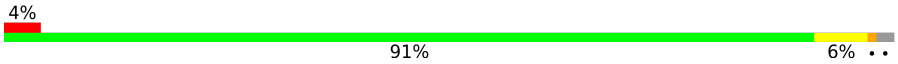
• Molecule 1: Pyruvate kinase

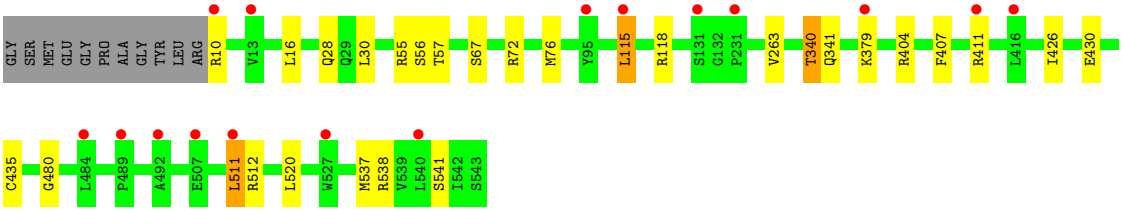
Chain A:



• Molecule 1: Pyruvate kinase

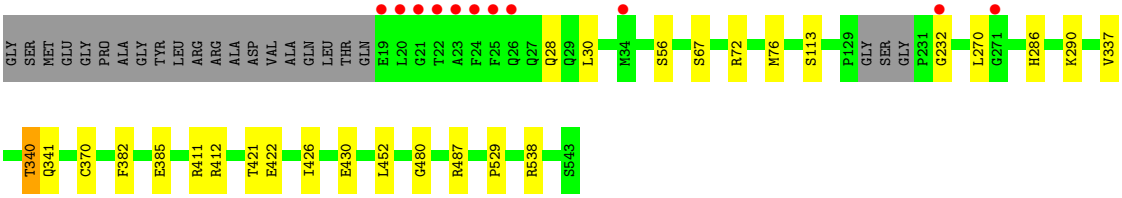
Chain B:





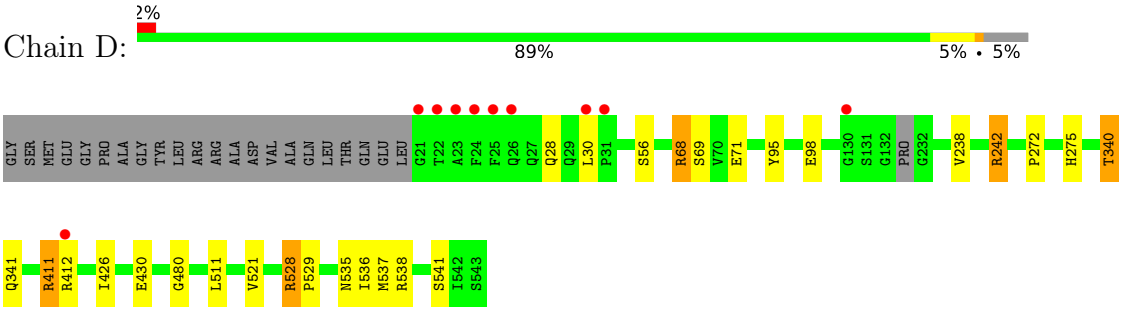
• Molecule 1: Pyruvate kinase

Chain C:



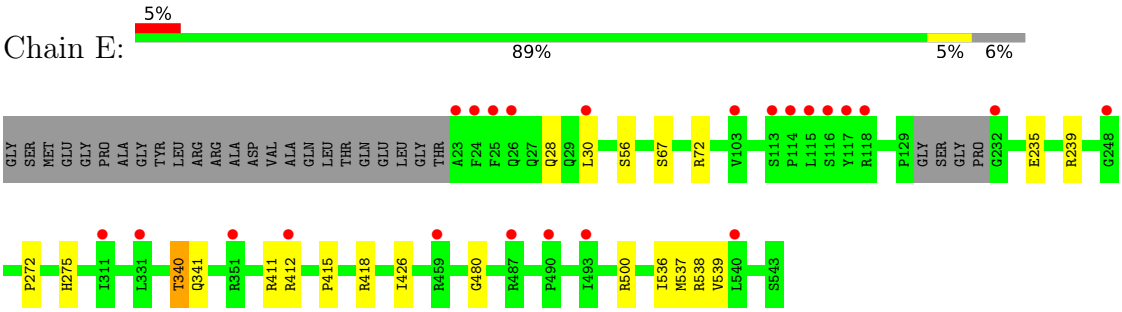
• Molecule 1: Pyruvate kinase

Chain D:



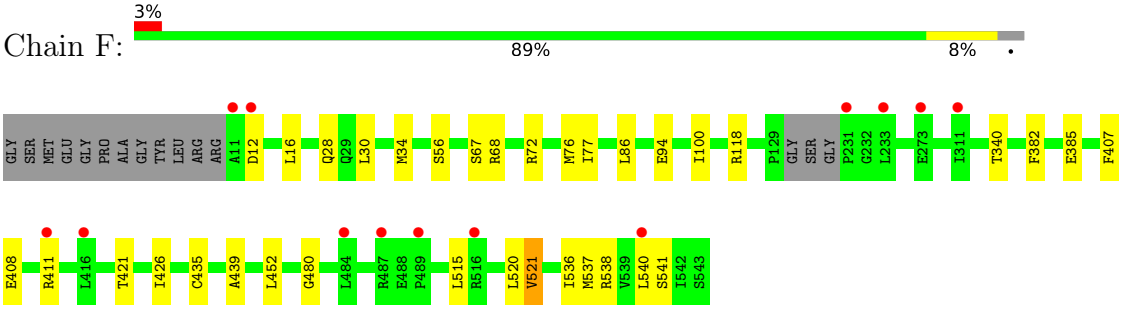
• Molecule 1: Pyruvate kinase

Chain E:



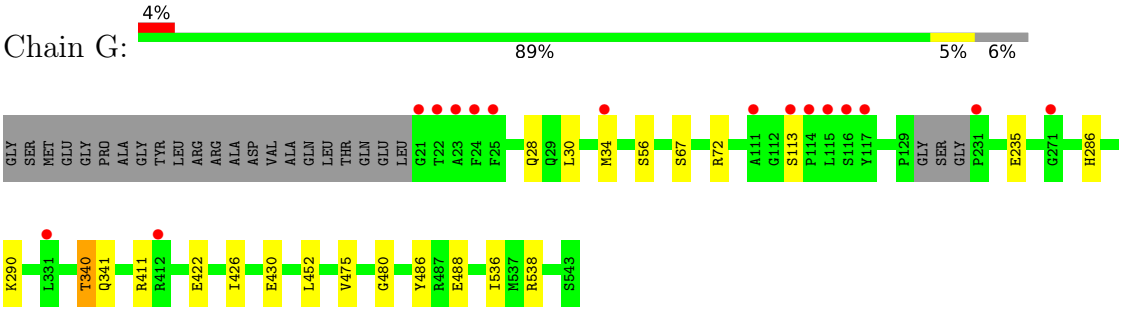
• Molecule 1: Pyruvate kinase

Chain F:



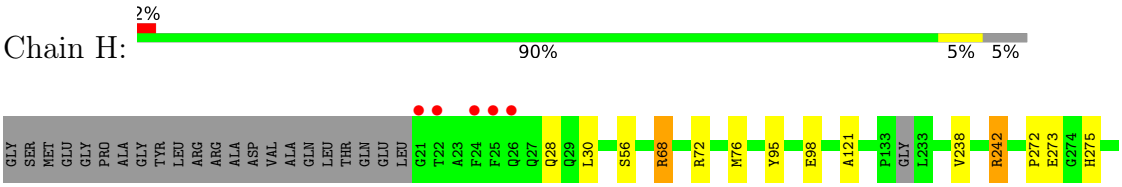
• Molecule 1: Pyruvate kinase

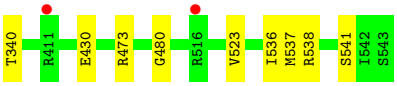
Chain G:



• Molecule 1: Pyruvate kinase

Chain H:




T340
R411
E430
R473
G480
R516
V523
I536
M537
R538
S541
I542
S543

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	207.06Å 112.75Å 188.33Å 90.00° 92.15° 90.00°	Depositor
Resolution (Å)	188.20 – 1.89 188.20 – 1.88	Depositor EDS
% Data completeness (in resolution range)	79.8 (188.20-1.89) 79.7 (188.20-1.88)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.42 (at 1.88Å)	Xtriage
Refinement program	BUSTER 2.10.4 (16-JUL-2021)	Depositor
R, R_{free}	0.202 , 0.226 0.194 , 0.217	Depositor DCC
R_{free} test set	13976 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	39.0	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 54.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	28866	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.35 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0048e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: FBP, OXL, MG, I8Q, K

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.36	0/3332	0.54	0/4502
1	B	0.37	0/3429	0.53	0/4636
1	C	0.44	0/3349	0.56	0/4527
1	D	0.46	0/3332	0.57	0/4502
1	E	0.36	0/3350	0.53	0/4527
1	F	0.41	0/3405	0.54	0/4603
1	G	0.46	0/3324	0.56	0/4493
1	H	0.49	0/3352	0.57	0/4529
All	All	0.42	0/26873	0.55	0/36319

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3242	0	3315	19	0
1	B	3350	0	3417	19	0
1	C	3268	0	3336	18	0
1	D	3254	0	3313	17	0
1	E	3257	0	3323	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3327	0	3399	21	0
1	G	3246	0	3308	15	0
1	H	3273	0	3337	15	0
2	A	20	0	10	0	0
2	B	20	0	10	0	0
2	C	20	0	10	0	0
2	D	20	0	10	0	0
2	E	20	0	10	0	0
2	F	20	0	10	0	0
2	G	20	0	10	0	0
2	H	20	0	10	0	0
3	A	6	0	0	0	0
3	B	6	0	0	0	0
3	C	6	0	0	0	0
3	D	6	0	0	0	0
3	E	6	0	0	0	0
3	F	6	0	0	0	0
3	G	6	0	0	0	0
3	H	6	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
6	C	22	9	0	0	0
6	F	22	9	0	0	0
6	G	22	9	0	0	0
7	A	179	0	0	0	0
7	B	209	0	0	0	0
7	C	333	0	0	2	0
7	D	368	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	E	195	0	0	0	0
7	F	286	0	0	0	0
7	G	359	0	0	0	0
7	H	403	0	0	0	0
All	All	28839	27	26828	119	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (119) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:411:ARG:HG3	1:C:426:ILE:HD11	1.57	0.85
1:C:422[A]:GLU:HG3	1:C:452:LEU:HD13	1.65	0.78
1:G:422[A]:GLU:HG3	1:G:452:LEU:HD13	1.69	0.75
1:E:418[B]:ARG:HG3	1:F:16:LEU:HD11	1.69	0.75
1:H:68:ARG:NH2	1:H:95:TYR:O	2.26	0.69
1:A:407:PHE:CE2	1:A:411:ARG:NH1	2.62	0.68
1:D:528:ARG:HD2	1:D:529:PRO:O	1.95	0.67
1:H:68:ARG:HH22	1:H:98:GLU:HB2	1.59	0.66
1:G:536:ILE:HG12	1:H:538[A]:ARG:HG2	1.78	0.65
1:F:411:ARG:HG3	1:F:426:ILE:HD11	1.79	0.64
1:A:536:ILE:HG12	1:B:538:ARG:HG2	1.78	0.64
1:F:407:PHE:CD2	1:F:411:ARG:NH1	2.66	0.63
1:D:68:ARG:NH2	1:D:95:TYR:O	2.32	0.62
1:A:418[B]:ARG:HG3	1:B:16:LEU:HD11	1.82	0.62
1:D:68:ARG:HH22	1:D:98:GLU:HB2	1.65	0.60
1:A:272:PRO:HA	1:A:275:HIS:NE2	2.16	0.60
1:A:67:SER:HA	1:A:72:ARG:HG2	1.84	0.59
1:H:56:SER:HB2	1:H:480:GLY:HA2	1.84	0.59
1:G:56:SER:HB2	1:G:480:GLY:HA2	1.84	0.59
1:A:272:PRO:HA	1:A:275:HIS:CE1	2.38	0.59
1:B:115:LEU:HA	1:B:512:ARG:HD2	1.83	0.59
1:G:411:ARG:HG3	1:G:426:ILE:HD11	1.84	0.58
1:B:407:PHE:CE2	1:B:411:ARG:NH1	2.71	0.58
1:B:56:SER:HB2	1:B:480:GLY:HA2	1.86	0.58
1:D:411:ARG:HG2	1:D:426:ILE:HD11	1.84	0.58
1:C:56:SER:HB2	1:C:480:GLY:HA2	1.86	0.58
1:F:407:PHE:CE2	1:F:411:ARG:NH1	2.72	0.58
1:F:56:SER:HB2	1:F:480:GLY:HA2	1.87	0.57
1:E:538:ARG:HG2	1:F:536:ILE:HG12	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:67:SER:HA	1:F:72:ARG:HG2	1.86	0.57
1:E:272:PRO:HA	1:E:275[A]:HIS:CE1	2.41	0.56
1:D:56:SER:HB2	1:D:480:GLY:HA2	1.88	0.56
1:E:536:ILE:HG12	1:F:538:ARG:HG2	1.87	0.56
1:B:411:ARG:HG2	1:B:426:ILE:HD11	1.88	0.56
1:H:272:PRO:HA	1:H:275[A]:HIS:CE1	2.40	0.56
1:E:235:GLU:O	1:E:239:ARG:HD3	2.06	0.55
1:D:272:PRO:HA	1:D:275[A]:HIS:CE1	2.41	0.55
1:D:69:SER:OG	1:D:71[B]:GLU:HG2	2.06	0.55
1:B:115:LEU:HA	1:B:512:ARG:CD	2.37	0.54
1:E:56:SER:HB2	1:E:480:GLY:HA2	1.89	0.54
1:C:67:SER:HA	1:C:72:ARG:HG2	1.90	0.54
1:E:411:ARG:HG3	1:E:426:ILE:HD11	1.88	0.54
1:A:412:ARG:NH1	1:B:404:ARG:HH11	2.07	0.53
1:C:538:ARG:HG2	1:D:536:ILE:HG12	1.91	0.53
1:G:486:TYR:CZ	1:G:488:GLU:HB2	2.44	0.53
1:E:67:SER:HA	1:E:72:ARG:HG2	1.90	0.53
1:G:67:SER:HA	1:G:72:ARG:HG2	1.91	0.53
1:C:538:ARG:HD3	7:C:861:HOH:O	2.09	0.52
1:C:232:GLY:HA3	7:C:913:HOH:O	2.09	0.52
1:B:407:PHE:CD2	1:B:411:ARG:NH1	2.78	0.52
1:B:67:SER:HA	1:B:72:ARG:HG2	1.92	0.51
1:A:115:LEU:HB2	1:A:511:LEU:HD21	1.92	0.50
1:H:68:ARG:NH2	1:H:98:GLU:HB2	2.24	0.50
1:H:72:ARG:O	1:H:76[B]:MET:HG2	2.14	0.48
1:H:56:SER:HB2	1:H:480:GLY:CA	2.44	0.48
1:B:115:LEU:CD1	1:B:511:LEU:HB3	2.44	0.48
1:C:430[B]:GLU:OE2	1:D:430[B]:GLU:OE1	2.32	0.47
1:F:28:GLN:HG3	1:F:30:LEU:HG	1.96	0.47
1:G:56:SER:HB2	1:G:480:GLY:CA	2.44	0.47
1:D:68:ARG:HD2	1:D:95:TYR:OH	2.15	0.47
1:B:28:GLN:HG3	1:B:30:LEU:HG	1.96	0.47
1:D:28:GLN:HG3	1:D:30:LEU:HG	1.98	0.46
1:H:238:VAL:O	1:H:242[B]:ARG:HG3	2.15	0.46
1:A:430:GLU:OE2	1:B:430[B]:GLU:OE1	2.33	0.46
1:A:110:PHE:HB3	1:A:116:SER:HB3	1.97	0.46
1:F:56:SER:HB2	1:F:480:GLY:CA	2.45	0.46
1:H:28:GLN:HG3	1:H:30:LEU:HG	1.98	0.46
1:C:56:SER:HB2	1:C:480:GLY:CA	2.46	0.46
1:E:28:GLN:HG3	1:E:30:LEU:HG	1.98	0.46
1:F:521:VAL:HG12	1:F:540[B]:LEU:HB3	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:SER:HB2	1:B:480:GLY:CA	2.46	0.45
1:C:28:GLN:HG3	1:C:30:LEU:HG	1.99	0.45
1:G:430[A]:GLU:OE1	1:H:430[A]:GLU:OE1	2.34	0.45
1:D:56:SER:HB2	1:D:480:GLY:CA	2.47	0.45
1:H:523:VAL:HB	1:H:538[B]:ARG:HG2	1.98	0.44
1:A:28:GLN:HG3	1:A:30:LEU:HG	2.00	0.44
1:G:28:GLN:HG3	1:G:30:LEU:HG	1.99	0.44
1:H:121:ALA:HA	1:H:473:ARG:HB3	1.99	0.44
1:F:77:ILE:CG2	1:F:118:ARG:HD3	2.47	0.44
1:F:77:ILE:HG22	1:F:118:ARG:HD3	2.00	0.44
1:F:382:PHE:HB3	1:F:385:GLU:HB2	1.99	0.44
1:G:538:ARG:HG2	1:H:536:ILE:HG12	2.00	0.44
1:D:238:VAL:O	1:D:242[B]:ARG:HG3	2.18	0.44
1:G:340:THR:HG22	1:G:341:GLN:HG3	2.00	0.44
1:A:443:LEU:HD22	1:A:525:THR:HG22	2.00	0.43
1:F:439:ALA:HB3	1:F:515:LEU:HD21	1.99	0.43
1:A:486:TYR:CZ	1:A:488[B]:GLU:HB2	2.54	0.43
1:F:435:CYS:HB2	1:F:520:LEU:HD12	2.01	0.43
1:C:529:PRO:HG3	1:G:235:GLU:HG2	2.00	0.43
1:D:340:THR:HG22	1:D:341:GLN:HG3	2.00	0.43
1:G:430[B]:GLU:OE2	1:H:430[B]:GLU:OE1	2.37	0.43
1:C:411:ARG:HH22	1:D:411:ARG:HH21	1.67	0.42
1:E:415:PRO:HB3	1:F:12:ASP:HA	2.01	0.42
1:G:286:HIS:CE1	1:G:290:LYS:HG3	2.55	0.42
1:A:340:THR:HG22	1:A:341:GLN:HG3	2.02	0.42
1:E:340:THR:HG22	1:E:341:GLN:HG3	2.01	0.42
1:A:430:GLU:OE2	1:B:430[A]:GLU:OE1	2.37	0.42
1:B:435:CYS:HB2	1:B:520:LEU:HD12	2.00	0.42
1:C:340:THR:HG22	1:C:341:GLN:HG3	2.02	0.42
1:B:340:THR:HG22	1:B:341:GLN:HG3	2.02	0.42
1:D:71[B]:GLU:CD	1:D:71[B]:GLU:H	2.23	0.42
1:C:286:HIS:CE1	1:C:290:LYS:HG3	2.55	0.42
1:A:382:PHE:HB3	1:A:385:GLU:HB2	2.02	0.42
1:C:337:VAL:HG22	1:C:370:CYS:HB2	2.02	0.42
1:D:535:ASN:OD1	1:D:536:ILE:HG13	2.20	0.41
1:E:56:SER:HB2	1:E:480:GLY:CA	2.49	0.41
1:F:86:LEU:HD11	1:F:100:ILE:HG12	2.02	0.41
1:F:421:THR:HG22	1:F:452:LEU:HD12	2.02	0.41
1:B:67:SER:HB2	1:B:76[B]:MET:SD	2.61	0.41
1:F:67:SER:HB2	1:F:76[B]:MET:SD	2.61	0.41
1:A:517:VAL:HG13	1:A:543:SER:HB3	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:30:LEU:O	1:G:34:MET:HG2	2.21	0.41
1:B:55:ARG:HD2	1:B:57:THR:O	2.21	0.41
1:C:67:SER:HB2	1:C:76[B]:MET:SD	2.61	0.41
1:F:30:LEU:O	1:F:34:MET:HG2	2.21	0.41
1:A:30:LEU:O	1:A:34:MET:HG2	2.22	0.40
1:C:382:PHE:HB3	1:C:385:GLU:HB2	2.04	0.40
1:A:407:PHE:HE2	1:A:411:ARG:HH12	1.61	0.40
1:C:421:THR:HG22	1:C:452:LEU:HD12	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	428/447 (96%)	424 (99%)	3 (1%)	1 (0%)	47	37
1	B	442/447 (99%)	436 (99%)	5 (1%)	1 (0%)	47	37
1	C	429/447 (96%)	424 (99%)	4 (1%)	1 (0%)	47	37
1	D	428/447 (96%)	424 (99%)	3 (1%)	1 (0%)	47	37
1	E	428/447 (96%)	424 (99%)	3 (1%)	1 (0%)	47	37
1	F	436/447 (98%)	432 (99%)	3 (1%)	1 (0%)	47	37
1	G	426/447 (95%)	419 (98%)	6 (1%)	1 (0%)	47	37
1	H	429/447 (96%)	423 (99%)	5 (1%)	1 (0%)	47	37
All	All	3446/3576 (96%)	3406 (99%)	32 (1%)	8 (0%)	47	37

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	340	THR
1	B	340	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	340	THR
1	D	340	THR
1	E	340	THR
1	F	340	THR
1	G	340	THR
1	H	340	THR

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	345/352 (98%)	340 (99%)	5 (1%)	67	62
1	B	353/352 (100%)	344 (98%)	9 (2%)	47	37
1	C	346/352 (98%)	341 (99%)	5 (1%)	67	62
1	D	343/352 (97%)	332 (97%)	11 (3%)	39	27
1	E	346/352 (98%)	341 (99%)	5 (1%)	67	62
1	F	351/352 (100%)	344 (98%)	7 (2%)	55	47
1	G	343/352 (97%)	341 (99%)	2 (1%)	86	86
1	H	345/352 (98%)	339 (98%)	6 (2%)	60	54
All	All	2772/2816 (98%)	2722 (98%)	50 (2%)	62	52

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	258	ARG
1	A	412	ARG
1	A	475	VAL
1	A	537[A]	MET
1	A	537[B]	MET
1	B	10	ARG
1	B	115	LEU
1	B	118	ARG
1	B	263	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	379	LYS
1	B	511	LEU
1	B	537[A]	MET
1	B	537[B]	MET
1	B	541	SER
1	C	113	SER
1	C	270[A]	LEU
1	C	270[B]	LEU
1	C	412	ARG
1	C	487	ARG
1	D	68	ARG
1	D	242[A]	ARG
1	D	242[B]	ARG
1	D	411	ARG
1	D	412	ARG
1	D	511	LEU
1	D	521	VAL
1	D	528	ARG
1	D	537	MET
1	D	538	ARG
1	D	541	SER
1	E	412	ARG
1	E	500	ARG
1	E	537[A]	MET
1	E	537[B]	MET
1	E	539	VAL
1	F	68	ARG
1	F	94	GLU
1	F	408	GLU
1	F	521	VAL
1	F	537[A]	MET
1	F	537[B]	MET
1	F	541	SER
1	G	113	SER
1	G	475	VAL
1	H	68	ARG
1	H	242[A]	ARG
1	H	242[B]	ARG
1	H	273	GLU
1	H	537	MET
1	H	541	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such

sidechains are listed below:

Mol	Chain	Res	Type
1	C	275	HIS
1	G	470	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 35 ligands modelled in this entry, 16 are monoatomic - leaving 19 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	I8Q	G	603	-	23,24,24	0.44	0	32,38,38	1.00	1 (3%)
2	FBP	D	601	-	18,20,20	0.49	0	23,32,32	1.16	1 (4%)
2	FBP	G	601	-	18,20,20	0.67	1 (5%)	23,32,32	0.81	0
3	OXL	B	602	4	0,5,5	-	-	0,6,6	-	-
3	OXL	D	602	4	0,5,5	-	-	0,6,6	-	-
3	OXL	F	602	4	0,5,5	-	-	0,6,6	-	-
3	OXL	H	602	4	0,5,5	-	-	0,6,6	-	-
2	FBP	C	601	-	18,20,20	0.68	1 (5%)	23,32,32	0.97	1 (4%)
3	OXL	E	602	4	0,5,5	-	-	0,6,6	-	-
3	OXL	A	602	4	0,5,5	-	-	0,6,6	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	FBP	E	601	-	18,20,20	0.60	0	23,32,32	0.91	1 (4%)
3	OXL	G	602	4	0,5,5	-	-	0,6,6	-	-
2	FBP	B	601	-	18,20,20	0.72	1 (5%)	23,32,32	0.93	1 (4%)
2	FBP	F	601	-	18,20,20	0.53	0	23,32,32	0.81	0
6	I8Q	F	603	-	23,24,24	0.28	0	32,38,38	0.88	1 (3%)
2	FBP	H	601	-	18,20,20	0.87	0	23,32,32	0.96	2 (8%)
6	I8Q	C	603	-	23,24,24	0.32	0	32,38,38	0.84	1 (3%)
3	OXL	C	602	4	0,5,5	-	-	0,6,6	-	-
2	FBP	A	601	-	18,20,20	0.41	0	23,32,32	0.88	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	I8Q	G	603	-	-	0/6/22/22	0/3/3/3
2	FBP	D	601	-	-	2/13/32/32	0/1/1/1
2	FBP	G	601	-	-	2/13/32/32	0/1/1/1
3	OXL	B	602	4	-	0/0/4/4	-
3	OXL	D	602	4	-	0/0/4/4	-
3	OXL	F	602	4	-	0/0/4/4	-
3	OXL	H	602	4	-	0/0/4/4	-
2	FBP	C	601	-	-	2/13/32/32	0/1/1/1
3	OXL	E	602	4	-	0/0/4/4	-
3	OXL	A	602	4	-	0/0/4/4	-
2	FBP	E	601	-	-	2/13/32/32	0/1/1/1
3	OXL	G	602	4	-	0/0/4/4	-
2	FBP	B	601	-	-	3/13/32/32	0/1/1/1
2	FBP	F	601	-	-	2/13/32/32	0/1/1/1
6	I8Q	F	603	-	-	0/6/22/22	0/3/3/3
2	FBP	H	601	-	-	2/13/32/32	0/1/1/1
6	I8Q	C	603	-	-	5/6/22/22	0/3/3/3
3	OXL	C	602	4	-	0/0/4/4	-
2	FBP	A	601	-	-	2/13/32/32	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	601	FBP	P2-O6P	-2.56	1.45	1.54
2	B	601	FBP	P2-O5P	-2.12	1.46	1.54
2	C	601	FBP	P1-O3P	-2.05	1.46	1.54

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	G	603	I8Q	C3-C-C1	-4.98	116.71	121.14
2	D	601	FBP	O5P-P2-O6	4.52	118.75	106.73
6	F	603	I8Q	C3-C-C1	-4.32	117.29	121.14
6	C	603	I8Q	C3-C-C1	-4.14	117.46	121.14
2	H	601	FBP	O5P-P2-O6	2.88	114.39	106.73
2	C	601	FBP	P1-O1-C1	2.86	126.17	118.30
2	E	601	FBP	O3P-P1-O2P	2.54	117.36	107.64
2	B	601	FBP	O3P-P1-O2P	2.43	116.91	107.64
2	H	601	FBP	O6P-P2-O5P	2.10	115.67	107.64

There are no chirality outliers.

All (22) torsion outliers are listed below:

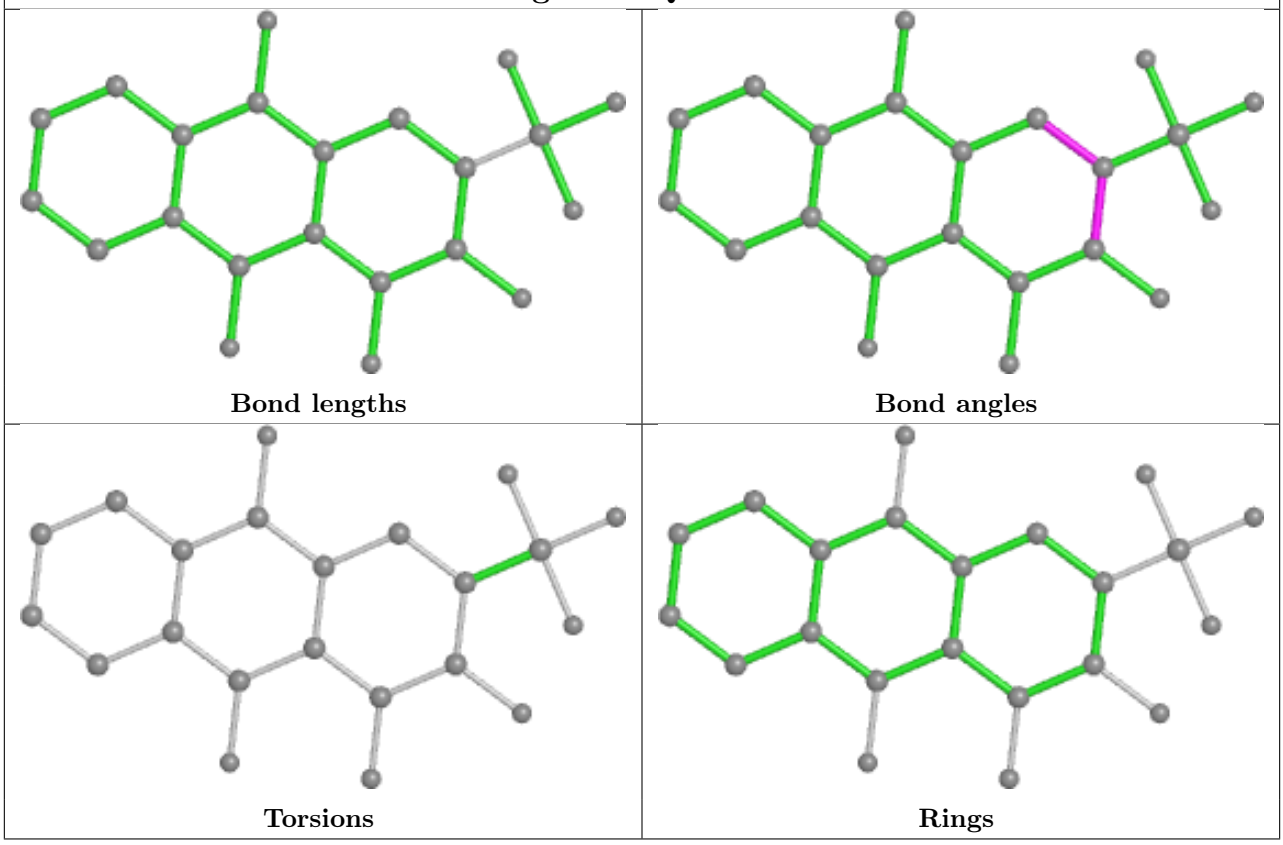
Mol	Chain	Res	Type	Atoms
2	A	601	FBP	C4-C5-C6-O6
2	B	601	FBP	C4-C5-C6-O6
2	C	601	FBP	C4-C5-C6-O6
2	D	601	FBP	C4-C5-C6-O6
2	E	601	FBP	C4-C5-C6-O6
2	H	601	FBP	C4-C5-C6-O6
2	F	601	FBP	C4-C5-C6-O6
2	G	601	FBP	C4-C5-C6-O6
2	A	601	FBP	O5-C5-C6-O6
2	C	601	FBP	O5-C5-C6-O6
2	B	601	FBP	O5-C5-C6-O6
2	D	601	FBP	O5-C5-C6-O6
2	E	601	FBP	O5-C5-C6-O6
2	F	601	FBP	O5-C5-C6-O6
2	G	601	FBP	O5-C5-C6-O6
2	H	601	FBP	O5-C5-C6-O6
2	B	601	FBP	C1-O1-P1-O1P
6	C	603	I8Q	C1-C-S-O5
6	C	603	I8Q	C1-C-S-O
6	C	603	I8Q	C1-C-S-O4
6	C	603	I8Q	C3-C-S-O5
6	C	603	I8Q	C3-C-S-O

There are no ring outliers.

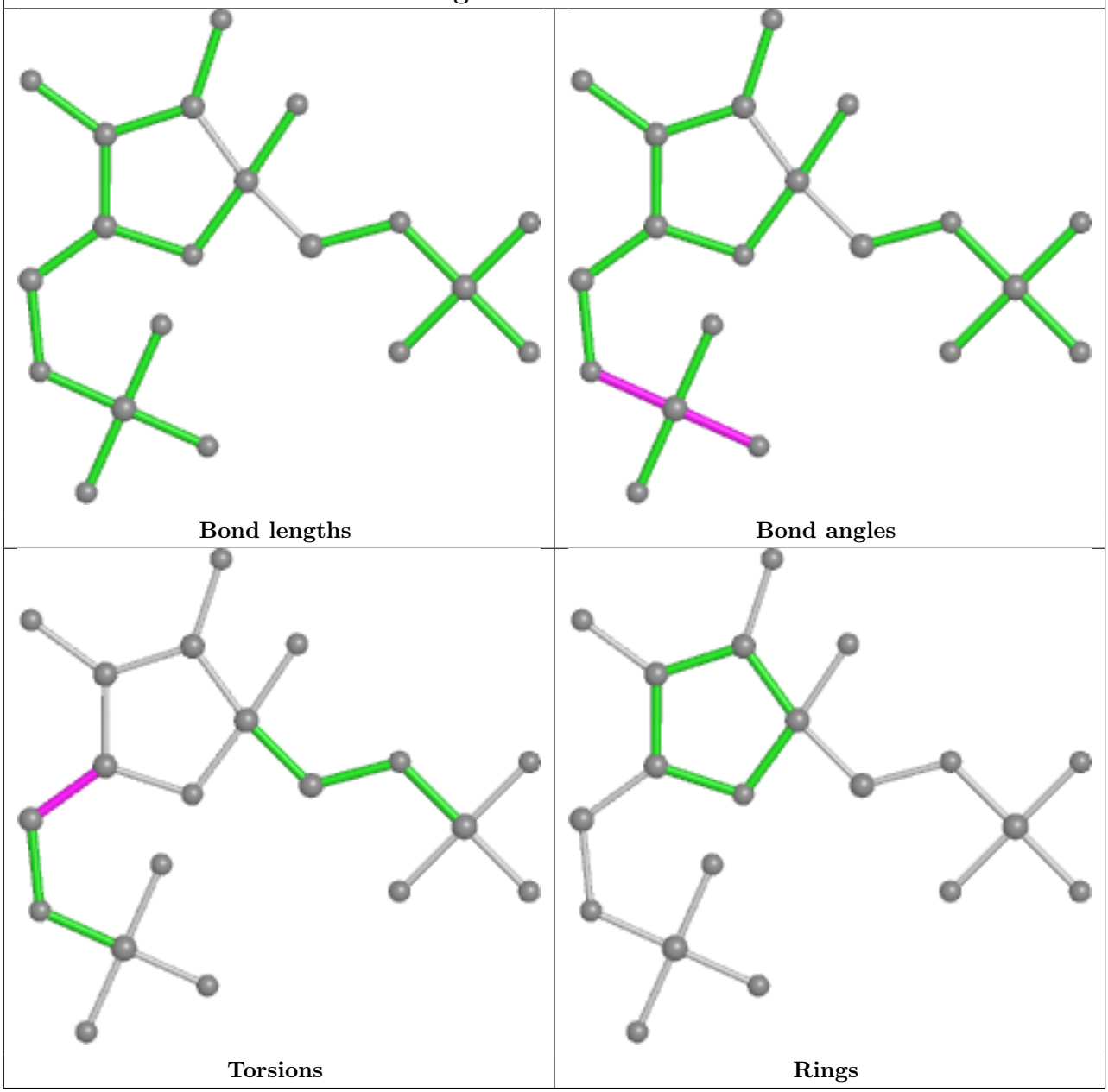
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

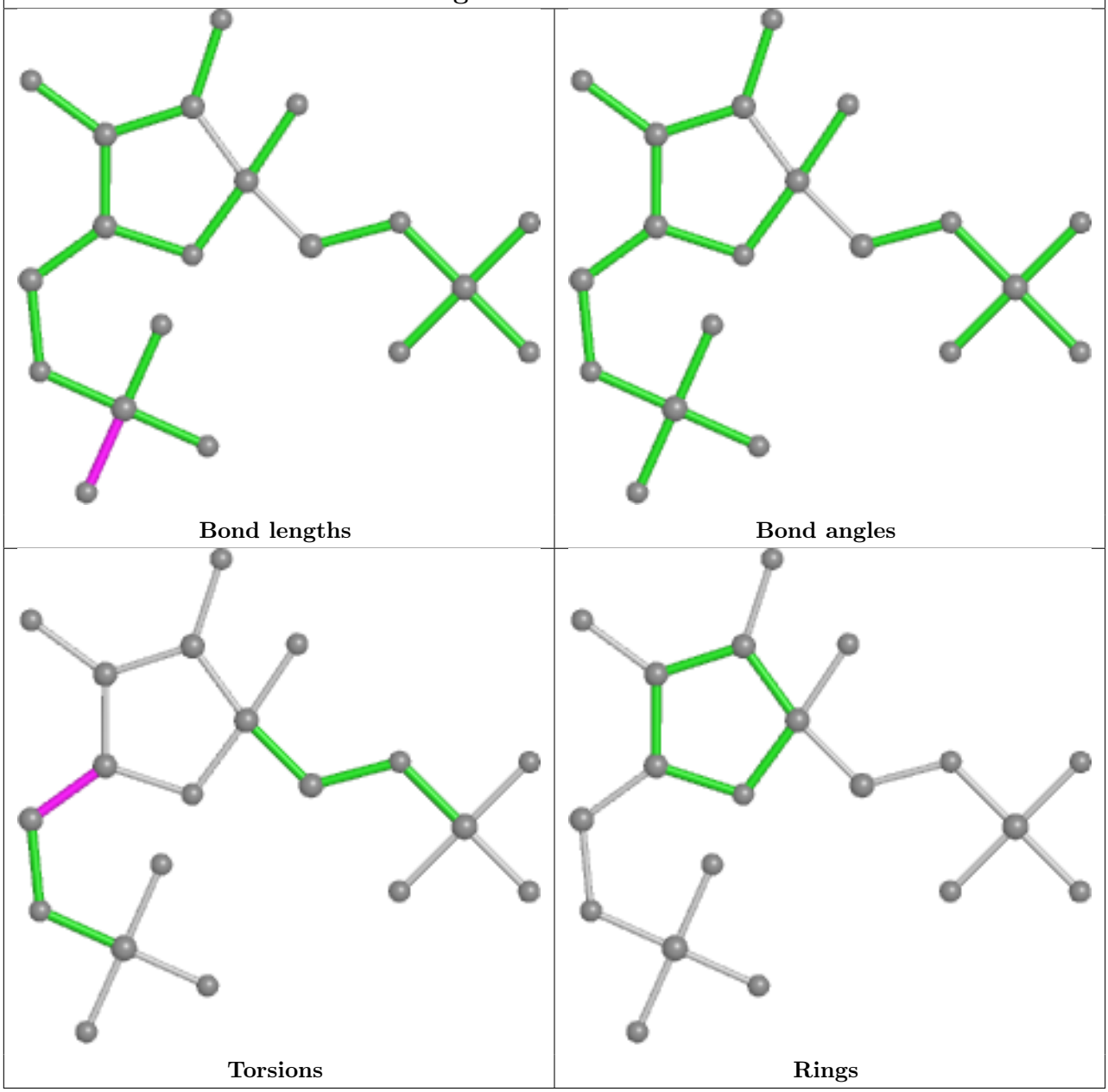
Ligand I8Q G 603



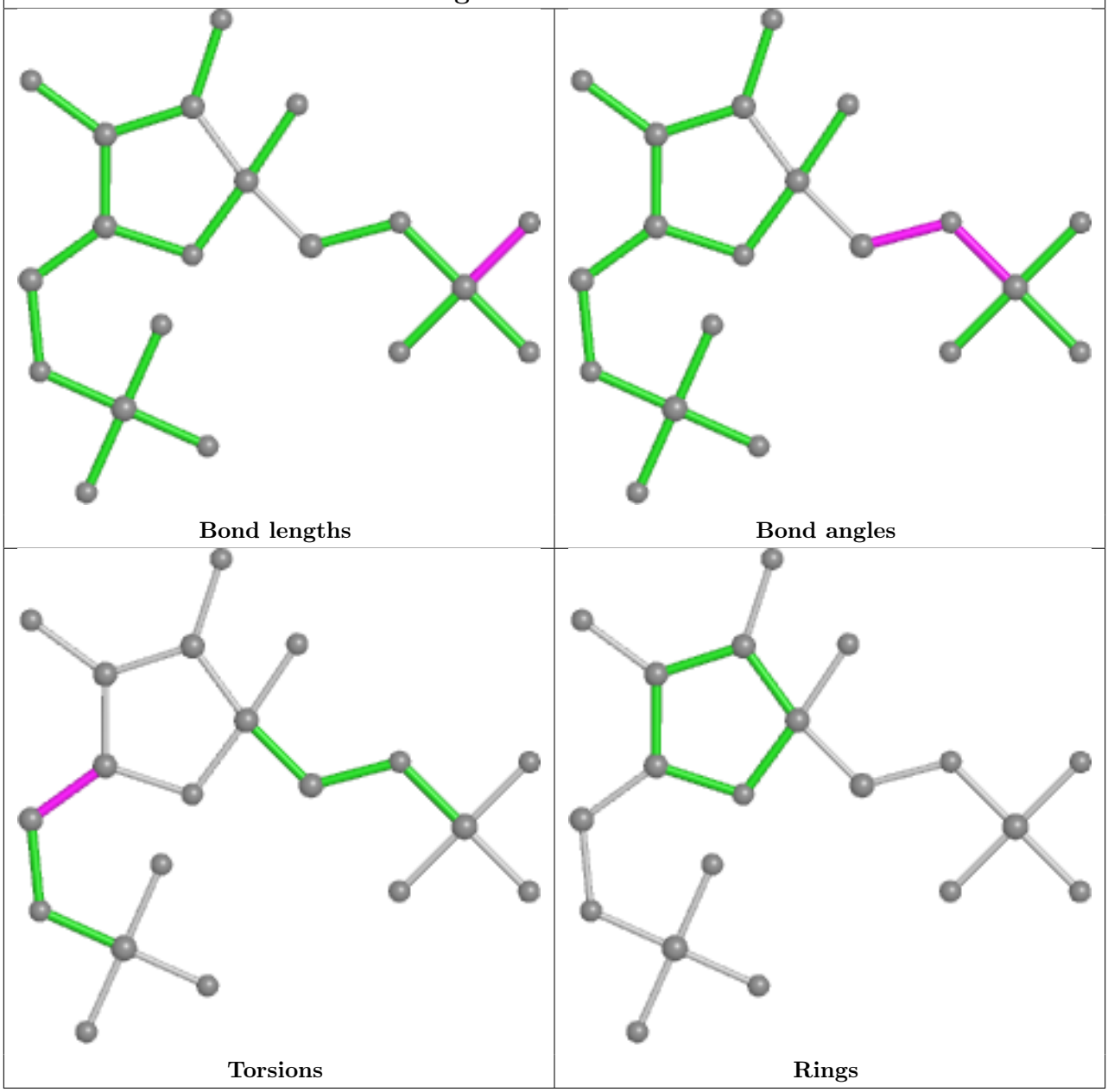
Ligand FBP D 601



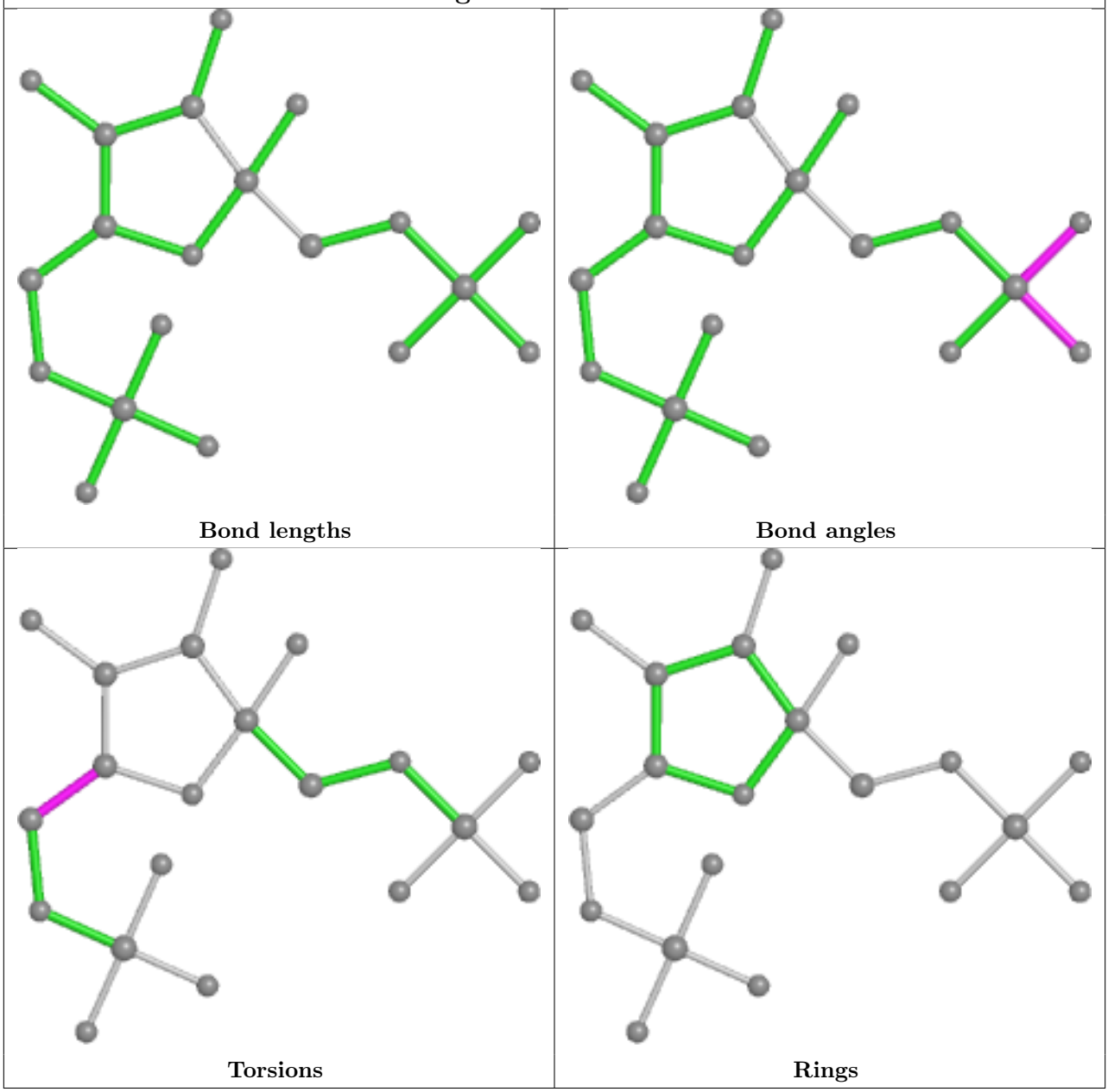
Ligand FBP G 601



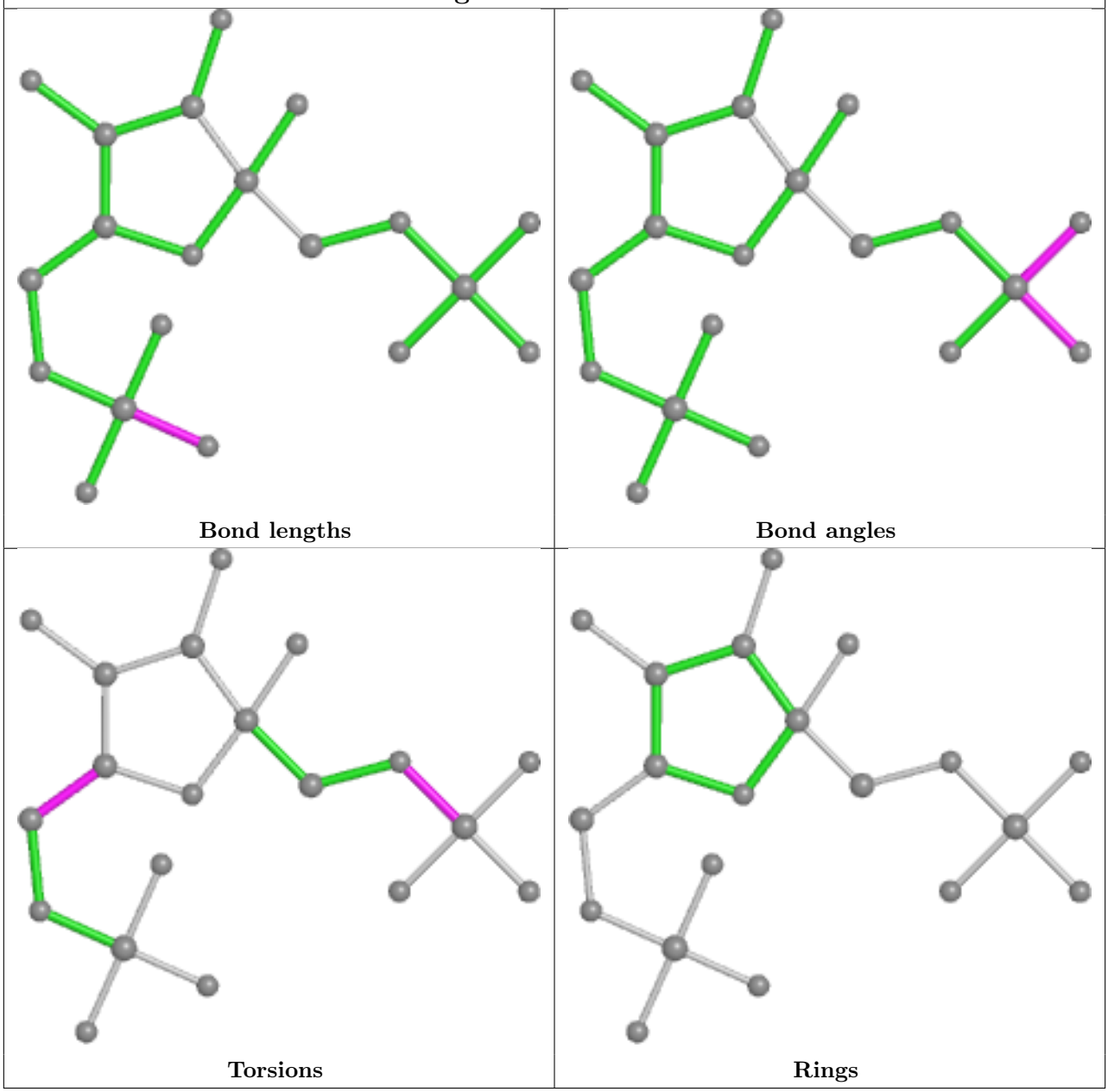
Ligand FBP C 601



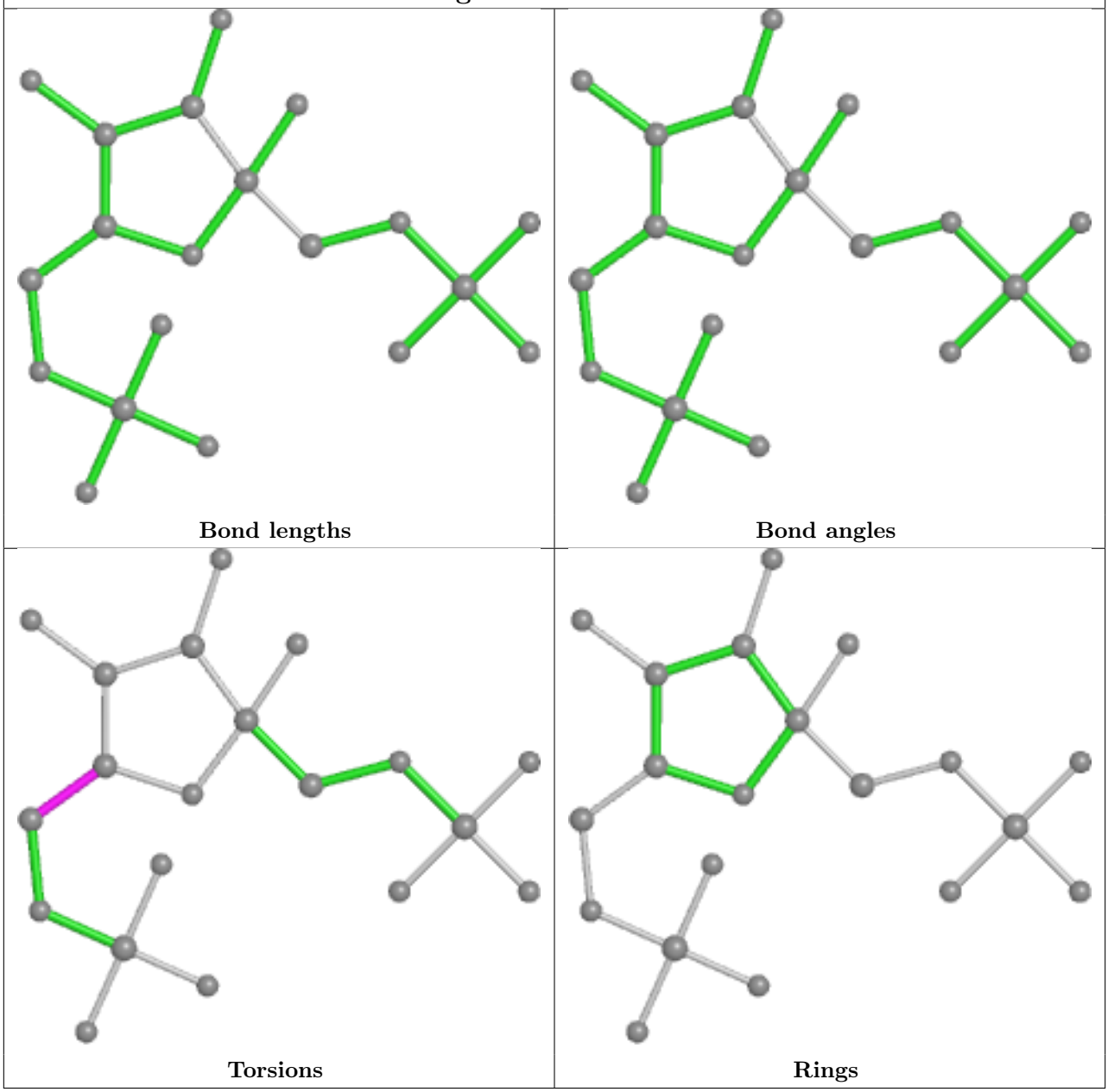
Ligand FBP E 601



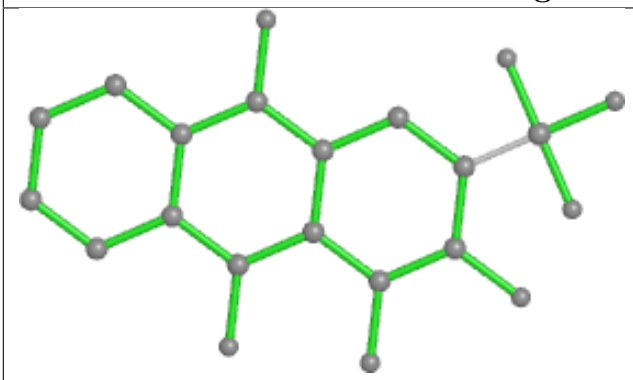
Ligand FBP B 601



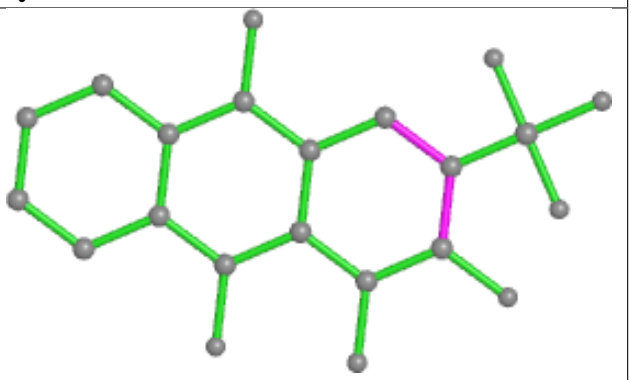
Ligand FBP F 601



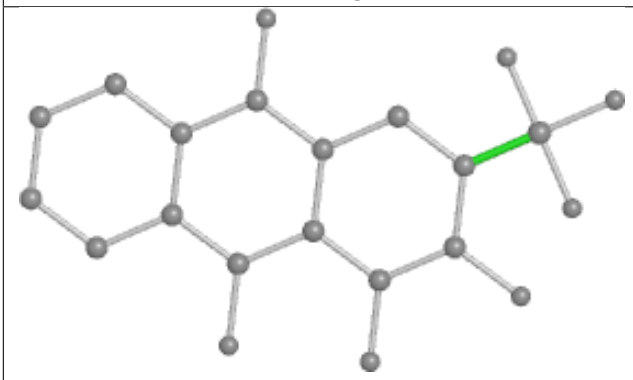
Ligand I8Q F 603



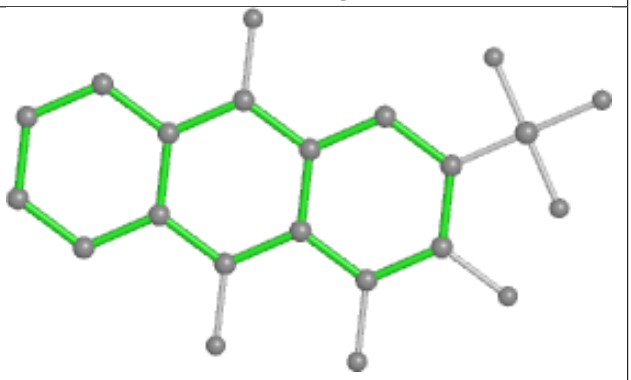
Bond lengths



Bond angles

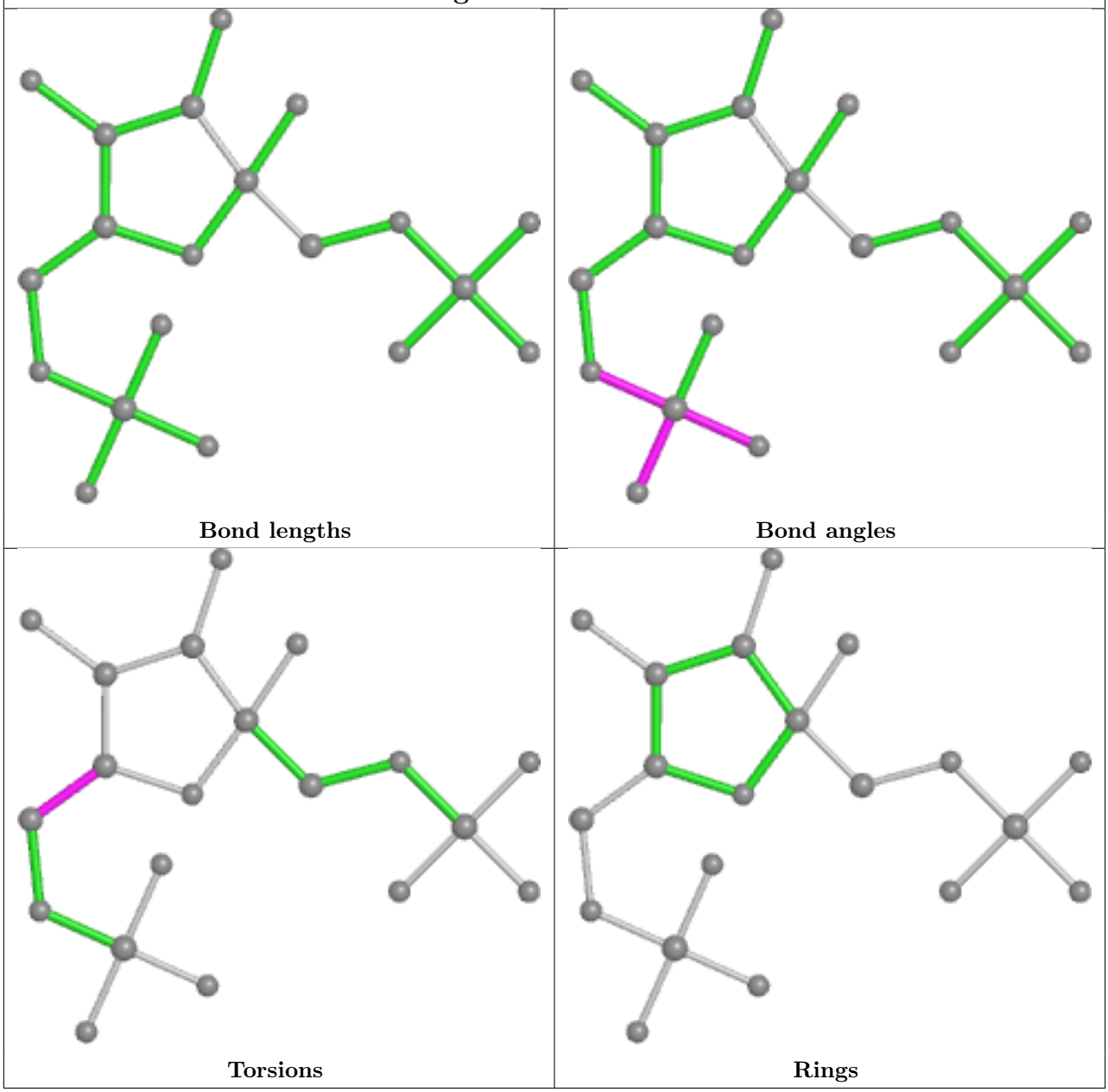


Torsions

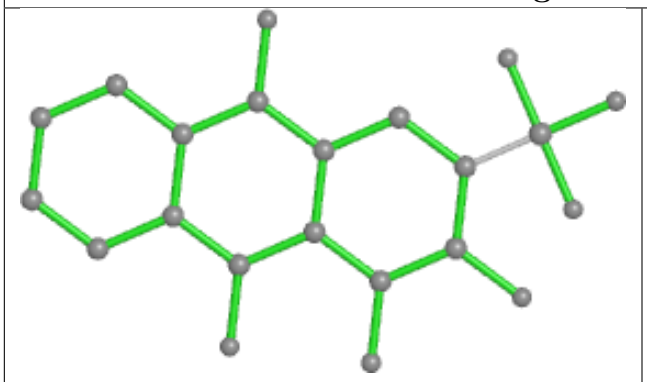


Rings

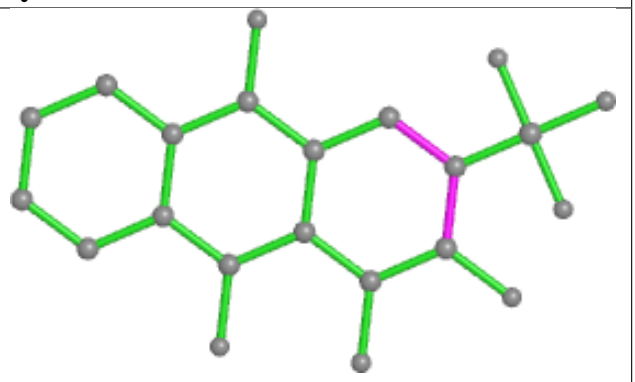
Ligand FBP H 601



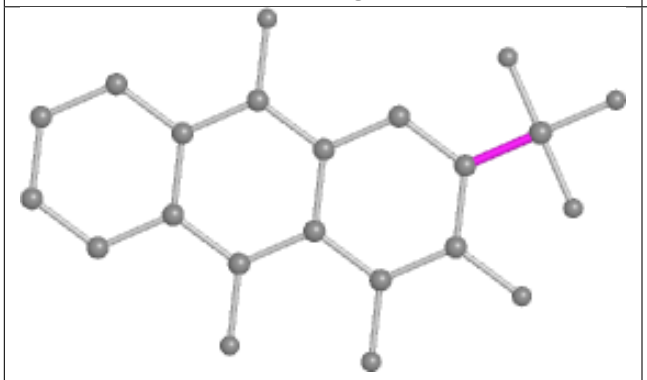
Ligand I8Q C 603



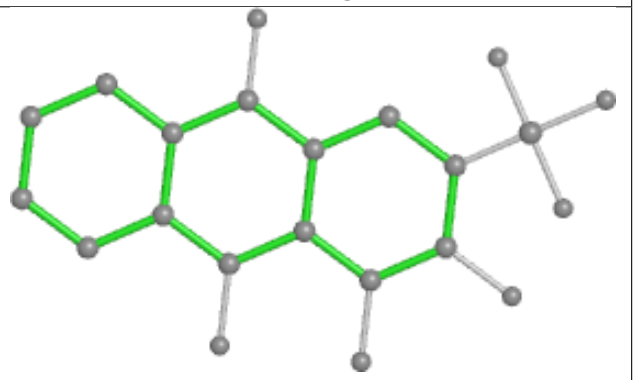
Bond lengths



Bond angles

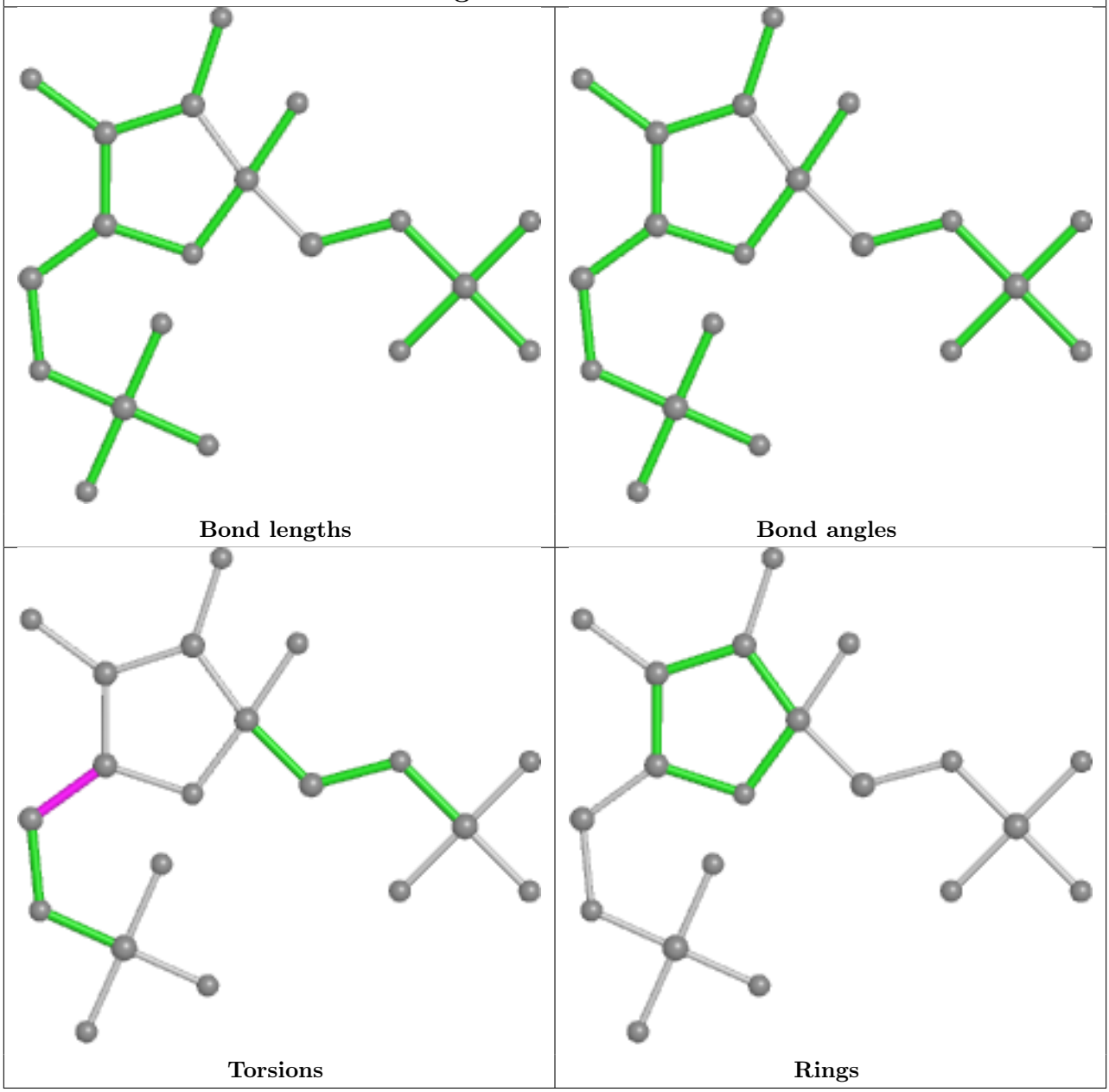


Torsions



Rings

Ligand FBP A 601



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	419/447 (93%)	0.55	35 (8%)	11	12	37, 53, 81, 93	0
1	B	436/447 (97%)	0.47	16 (3%)	41	43	31, 50, 76, 89	0
1	C	424/447 (94%)	0.24	11 (2%)	56	57	27, 40, 63, 117	0
1	D	424/447 (94%)	0.30	10 (2%)	59	60	27, 36, 61, 109	0
1	E	419/447 (93%)	0.53	23 (5%)	25	26	34, 52, 81, 94	0
1	F	432/447 (96%)	0.25	13 (3%)	50	51	26, 44, 66, 84	0
1	G	422/447 (94%)	0.26	16 (3%)	40	42	26, 36, 57, 101	1 (0%)
1	H	424/447 (94%)	0.24	7 (1%)	70	72	25, 33, 55, 99	0
All	All	3400/3576 (95%)	0.35	131 (3%)	39	41	25, 44, 73, 117	1 (0%)

All (131) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	21	GLY	12.7
1	D	24	PHE	12.6
1	D	25	PHE	12.5
1	D	22	THR	12.2
1	E	25	PHE	11.6
1	E	115	LEU	10.3
1	C	22	THR	8.6
1	G	22	THR	8.2
1	C	21	GLY	7.7
1	H	25	PHE	7.5
1	C	20	LEU	7.4
1	A	115	LEU	7.0
1	E	24	PHE	6.8
1	D	21	GLY	6.7
1	G	25	PHE	6.7
1	A	30	LEU	6.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	543	SER	6.0
1	G	21	GLY	6.0
1	E	114	PRO	5.9
1	H	22	THR	5.6
1	H	24	PHE	5.5
1	A	113	SER	5.3
1	A	116	SER	5.3
1	E	113	SER	5.1
1	B	511	LEU	4.9
1	C	25	PHE	4.6
1	E	30	LEU	4.6
1	G	271	GLY	4.6
1	A	63	ILE	4.4
1	A	34	MET	4.4
1	D	30	LEU	4.3
1	F	489	PRO	4.3
1	A	114	PRO	4.2
1	D	26	GLN	4.2
1	G	115	LEU	4.1
1	B	13	VAL	4.1
1	E	26	GLN	4.0
1	B	115	LEU	3.9
1	B	489	PRO	3.8
1	E	103	VAL	3.8
1	G	331	LEU	3.5
1	B	527	TRP	3.5
1	A	33	ALA	3.5
1	A	112	GLY	3.5
1	D	23	ALA	3.5
1	E	116	SER	3.4
1	F	11	ALA	3.4
1	B	540[A]	LEU	3.4
1	C	23	ALA	3.4
1	B	10	ARG	3.3
1	H	516	ARG	3.3
1	G	24	PHE	3.3
1	B	95	TYR	3.2
1	A	275	HIS	3.2
1	E	23	ALA	3.1
1	F	516	ARG	3.0
1	A	527	TRP	3.0
1	E	540	LEU	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	231	PRO	3.0
1	C	271	GLY	2.9
1	F	12	ASP	2.9
1	G	23	ALA	2.9
1	A	412	ARG	2.8
1	E	248	GLY	2.8
1	E	232	GLY	2.7
1	G	114	PRO	2.7
1	G	34	MET	2.7
1	G	412	ARG	2.7
1	B	507	GLU	2.7
1	D	31	PRO	2.7
1	A	500	ARG	2.7
1	A	91	GLY	2.6
1	A	108	GLU	2.6
1	A	511	LEU	2.6
1	F	484	LEU	2.6
1	A	248	GLY	2.6
1	B	416	LEU	2.5
1	C	19	GLU	2.5
1	F	487	ARG	2.5
1	E	490	PRO	2.5
1	G	231	PRO	2.5
1	C	24	PHE	2.5
1	G	117	TYR	2.5
1	C	34	MET	2.4
1	D	412	ARG	2.4
1	A	273	GLU	2.4
1	F	540[A]	LEU	2.4
1	A	499[A]	ASP	2.4
1	A	31	PRO	2.4
1	B	131	SER	2.4
1	C	232	GLY	2.4
1	G	116	SER	2.4
1	C	26	GLN	2.4
1	A	495	ALA	2.3
1	A	459	ARG	2.3
1	E	117	TYR	2.3
1	H	26	GLN	2.3
1	E	331	LEU	2.3
1	A	242	ARG	2.3
1	A	493	ILE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	408[A]	GLU	2.3
1	F	231	PRO	2.2
1	B	492	ALA	2.2
1	E	487	ARG	2.2
1	A	124	LEU	2.2
1	A	271	GLY	2.2
1	E	118	ARG	2.2
1	E	412	ARG	2.2
1	A	489	PRO	2.2
1	A	407	PHE	2.2
1	A	482	PHE	2.2
1	B	379	LYS	2.2
1	E	311	ILE	2.1
1	A	411	ARG	2.1
1	F	273	GLU	2.1
1	F	416	LEU	2.1
1	G	113	SER	2.1
1	E	459	ARG	2.1
1	F	311	ILE	2.1
1	B	484	LEU	2.1
1	G	111	ALA	2.1
1	B	411	ARG	2.1
1	A	71	GLU	2.1
1	F	233	LEU	2.1
1	H	411	ARG	2.0
1	D	130	GLY	2.0
1	E	351	ARG	2.0
1	E	493	ILE	2.0
1	A	26	GLN	2.0
1	A	86	LEU	2.0
1	F	411	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

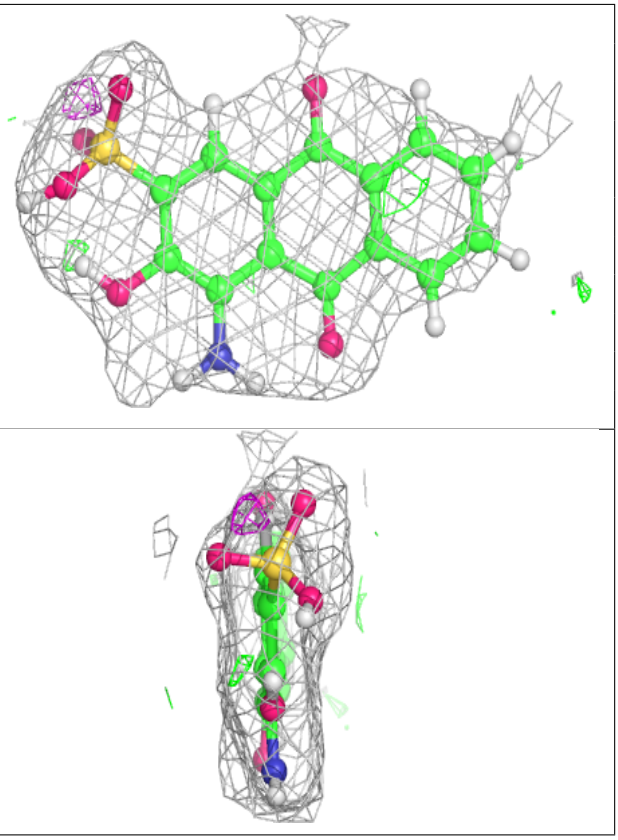
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	K	A	604	1/1	0.73	0.10	91,91,91,91	0
3	OXL	E	602	6/6	0.89	0.17	57,57,57,57	0
5	K	E	604	1/1	0.89	0.28	87,87,87,87	0
6	I8Q	C	603	22/22	0.89	0.13	70,71,71,71	9
4	MG	A	603	1/1	0.90	0.06	54,54,54,54	0
5	K	D	604	1/1	0.92	0.07	49,49,49,49	0
5	K	B	604	1/1	0.93	0.09	73,73,73,73	0
4	MG	E	603	1/1	0.93	0.07	49,49,49,49	0
6	I8Q	F	603	22/22	0.93	0.21	58,62,64,64	9
6	I8Q	G	603	22/22	0.93	0.11	55,57,59,59	9
4	MG	B	603	1/1	0.94	0.07	51,51,51,51	0
3	OXL	A	602	6/6	0.94	0.17	55,55,55,55	0
3	OXL	B	602	6/6	0.94	0.09	45,45,47,47	0
2	FBP	E	601	20/20	0.95	0.12	45,46,47,48	0
3	OXL	G	602	6/6	0.95	0.11	39,40,41,41	0
4	MG	C	604	1/1	0.96	0.09	46,46,46,46	0
3	OXL	D	602	6/6	0.96	0.10	37,39,39,39	0
5	K	F	605	1/1	0.96	0.06	70,70,70,70	0
2	FBP	F	601	20/20	0.96	0.10	40,44,49,49	0
3	OXL	F	602	6/6	0.96	0.13	43,44,45,46	0
5	K	C	605	1/1	0.96	0.10	58,58,58,58	0
2	FBP	A	601	20/20	0.97	0.11	45,47,47,48	0
2	FBP	B	601	20/20	0.97	0.11	46,47,51,51	0
4	MG	F	604	1/1	0.97	0.06	39,39,39,39	0
2	FBP	G	601	20/20	0.98	0.12	26,28,30,30	0
5	K	H	604	1/1	0.98	0.06	50,50,50,50	0
3	OXL	C	602	6/6	0.98	0.08	47,48,48,49	0
4	MG	H	603	1/1	0.98	0.10	38,38,38,38	0
3	OXL	H	602	6/6	0.98	0.09	32,33,34,34	0
4	MG	D	603	1/1	0.99	0.07	37,37,37,37	0
5	K	G	605	1/1	0.99	0.07	55,55,55,55	0
2	FBP	H	601	20/20	0.99	0.13	24,25,29,29	0
2	FBP	D	601	20/20	0.99	0.12	27,29,31,32	0
4	MG	G	604	1/1	0.99	0.11	35,35,35,35	0
2	FBP	C	601	20/20	0.99	0.12	27,30,34,35	0

The following is a graphical depiction of the model fit to experimental electron density of all

instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

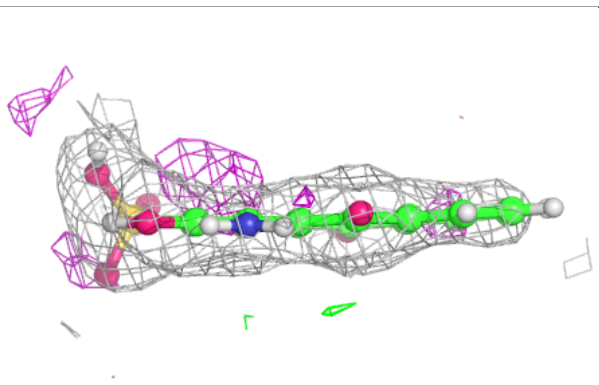
Electron density around I8Q C 603:

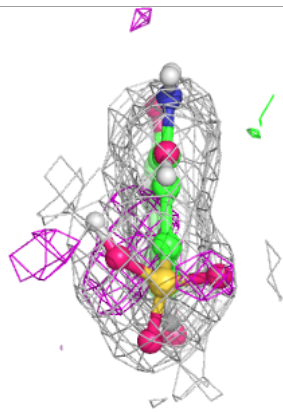
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around I8Q F 603:

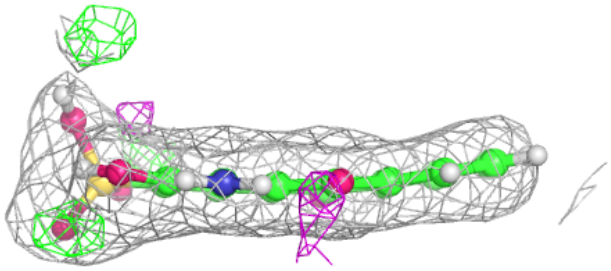
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

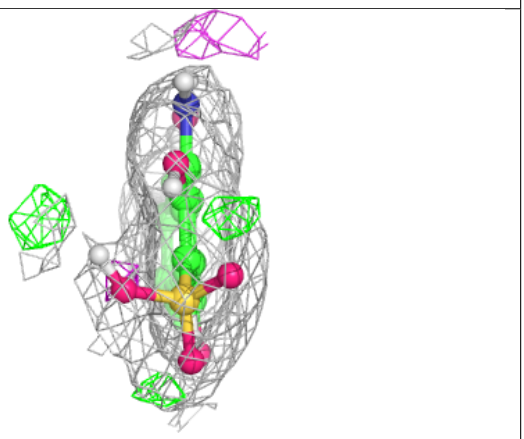




Electron density around I8Q G 603:

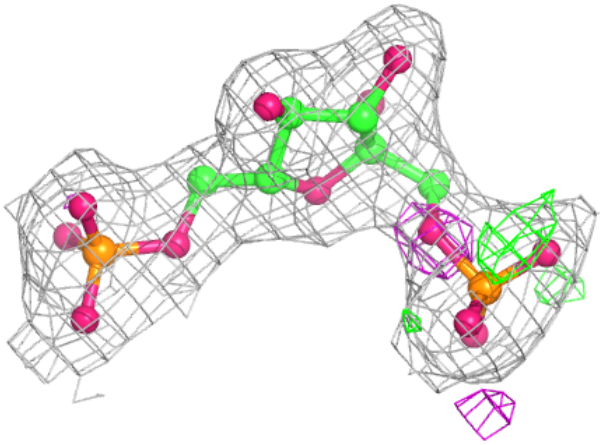
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

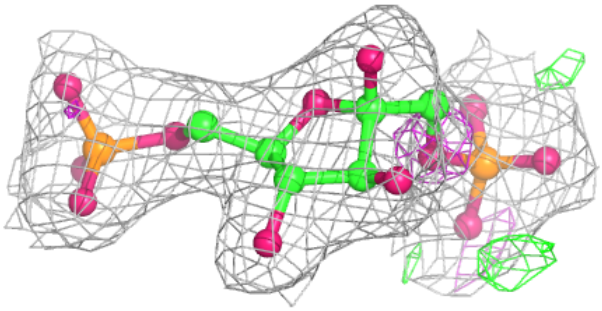


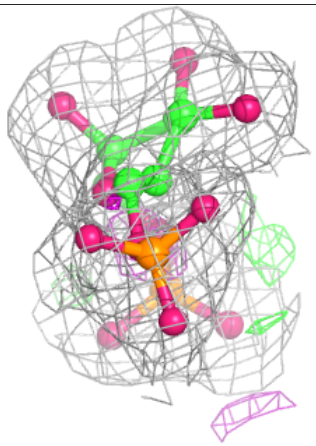


Electron density around FBP E 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

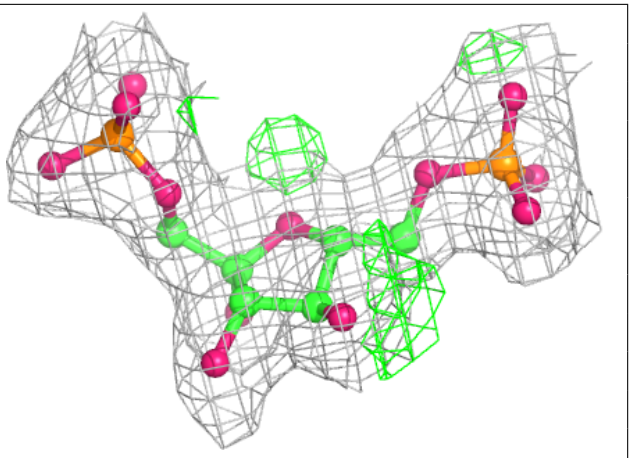


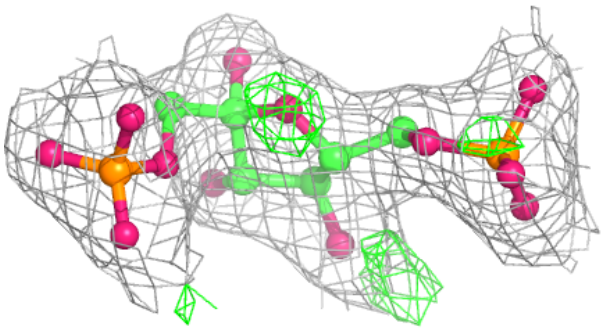


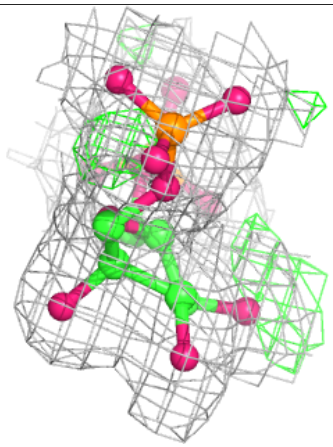


Electron density around FBP F 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

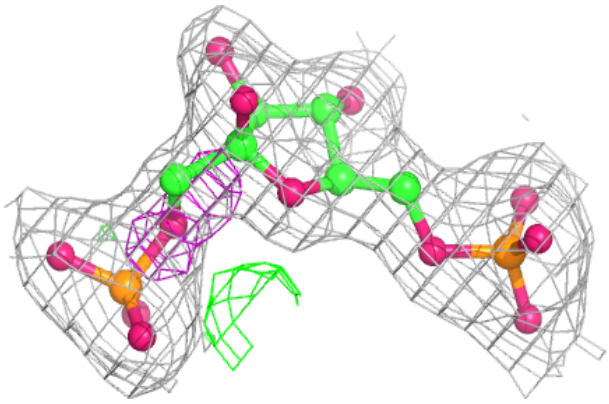


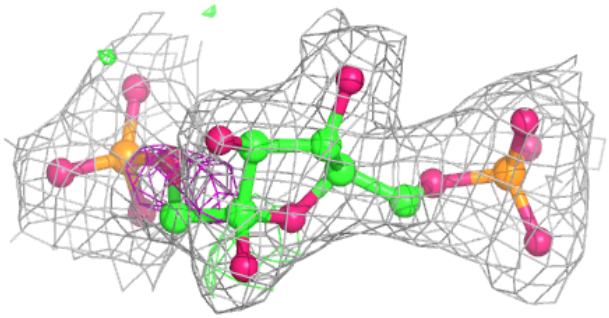


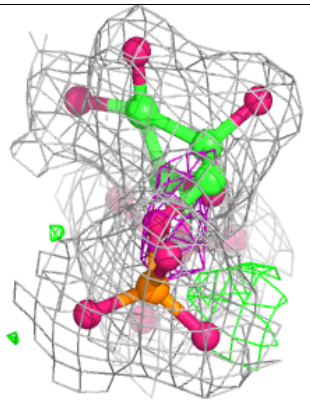


Electron density around FBP A 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

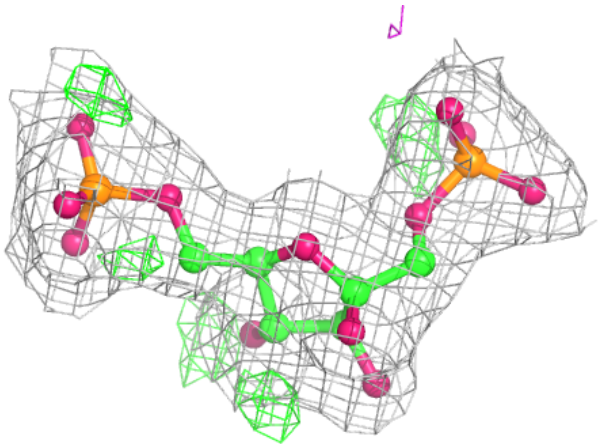


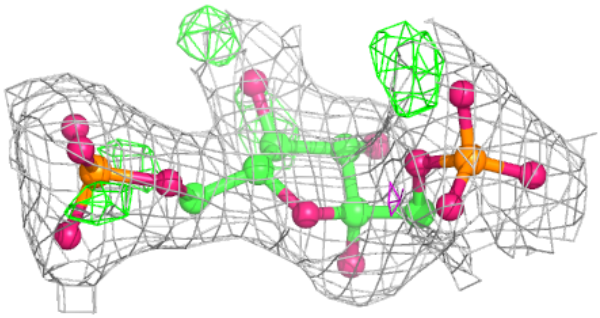


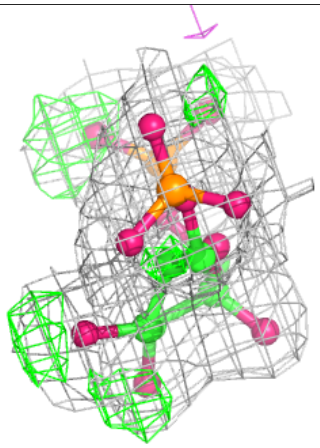


Electron density around FBP B 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

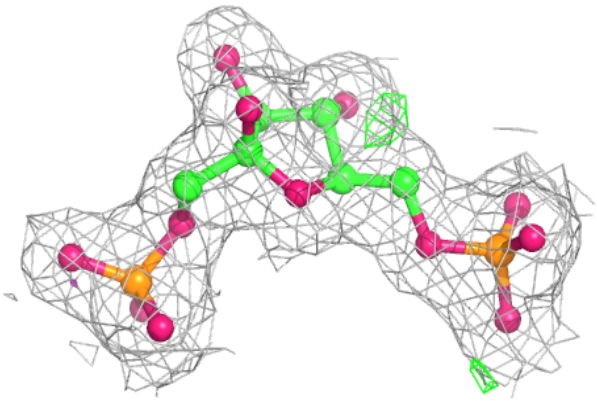


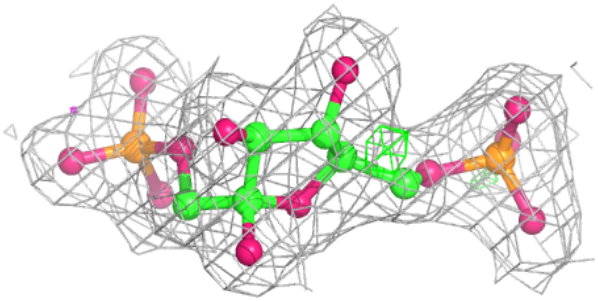




Electron density around FBP G 601:

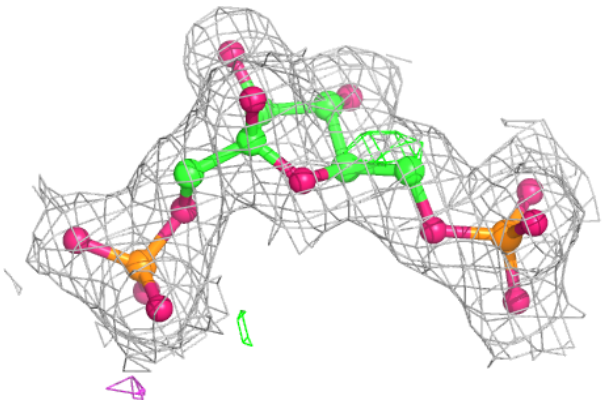
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

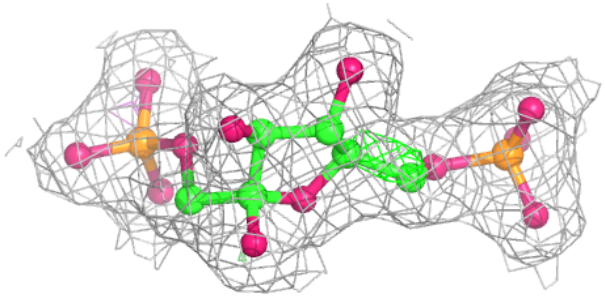




Electron density around FBP H 601:

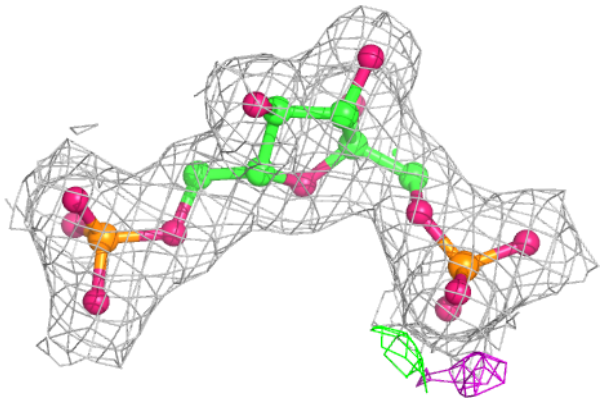
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

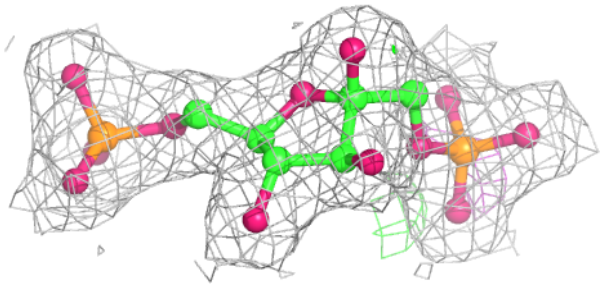


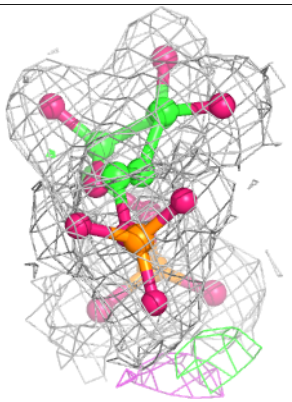


Electron density around FBP D 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

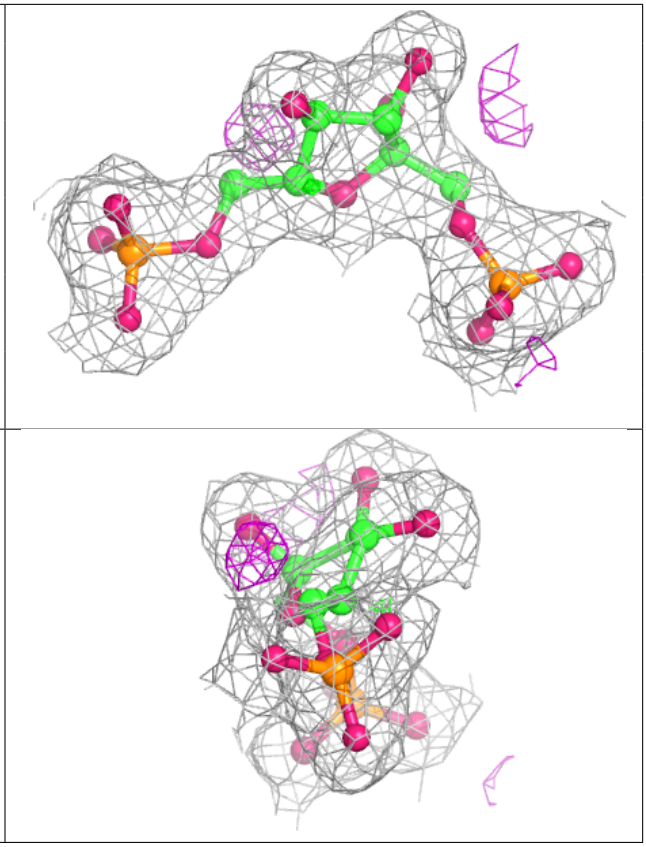






Electron density around FBP C 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.